



1652

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/644,668A

DATE: 04/29/2002
 TIME: 15:09:40

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#13
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 P.2.

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3 <110> APPLICANT: Korman, Alan J.
 4 Halk, Edward L.
 5 Lonberg, Nils
 6 Medarex, Inc.
 8 <120> TITLE OF INVENTION: Human CTLA-4 Antibodies and Their Uses
 10 <130> FILE REFERENCE: 014643-010510US
 12 <140> CURRENT APPLICATION NUMBER: US 09/644,668A
 13 <141> CURRENT FILING DATE: 2000-08-24
 15 <150> PRIOR APPLICATION NUMBER: US 60/150,452
 16 <151> PRIOR FILING DATE: 1999-08-24
 18 <160> NUMBER OF SEQ ID NOS: 41
 20 <170> SOFTWARE: PatentIn Ver. 2.1
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 3159
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Artificial Sequence
 27 <220> FEATURE:
 28 <223> OTHER INFORMATION: Description of Artificial Sequence:cloning vector
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 34 aaagcccgcg cattaggcgg gctcttgga gaacatatcc atcgcgtccg ccatctccag 180
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 40 acctacatct gtattaacga agcgtggca ttgacctga gtgatttttc tctgggtccc 540
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 42 atcagtaacc cgtatcgtga gcatcctctc tcgtttcatc ggtatcatta ccccatgaa 660
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 44 atggcccgcg ttatcagaag ccagacatta acgcttcttg agaaactcaa cgagctggac 780
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82 tcatgagcgg atacatattt gaatgtattt agaaaaataa acaaataggg gttccgcgca 3060
83 catttccccg aaaagtgcc cctgacgtct aagaaacat tattatcatg acattaacct 3120
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87 <210> SEQ ID NO: 2

88 <211> LENGTH: 349

89 <212> TYPE: DNA

90 <213> ORGANISM: Homo sapiens

92 <220> FEATURE:

93 <223> OTHER INFORMATION: preliminary sequence for heavy chain fragment

94 10D1.3

96 <400> SEQUENCE: 2

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97 tgggggaggg gtggtccagc ctgggaggtc cctgagactc tctgtgcag cctctggatt 60
98 cacttccagt agctatacta tgactgggt ccgccaggct ccaggcaagg ggtctggagt 120
99 ggtgacattt atatcatatg atggaaacaa taaatactac gcagactccg tgaagggccg 180
100 attcaccatc tccagagaca attccaagaa cagcgtgtat ctgcaaatga acagcctgag 240
101 agctgaggac acggctatat attactgtgc gaggaccggc tggctggggc cctttgacta 300
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105 <210> SEQ ID NO: 3

106 <211> LENGTH: 321

107 <212> TYPE: DNA

108 <213> ORGANISM: Homo sapiens

110 <220> FEATURE:

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111 <223> OTHER INFORMATION: preliminary sequence for light chain fragment
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114 <400> SEQUENCE: 3
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116 agagtgttgg cagcagctac ttagcctggg accagcagaa acctggccag gctcccaggc 120
117 tctcatctta tgggtgcattc agcagggcca ctggcatccc agacaggttc agtggcagtg 180
118 ggtctgggac agacttcact ctcaccatca gcagactgga gcctgaagat tttgcagtgt 240
119 attactgtca gcagtatggg agctcaccgt ggacgttcgg ccaagggacc aaggtggaaa 300
120 tcaaacgaac tgtggctgca c                                     321
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124 <211> LENGTH: 287
125 <212> TYPE: DNA
126 <213> ORGANISM: Homo sapiens
128 <220> FEATURE:
129 <223> OTHER INFORMATION: Vk A-27 germline sequence
131 <400> SEQUENCE: 4
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134 cctggccagg ctcccaggct cctcatctat ggtgcattca gcagggccac tggcatccca 180
135 gacaggttca gtggcagtggt gtctgggaca gacttcactc tcaccatcag cagactggag 240
136 cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcacc          287
139 <210> SEQ ID NO: 5
140 <211> LENGTH: 95
141 <212> TYPE: PRT
142 <213> ORGANISM: Homo sapiens
144 <220> FEATURE:
145 <223> OTHER INFORMATION: light chain variable region predicted sequence for
146     Vk A-27 germline
148 <400> SEQUENCE: 5
149 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
150   1           5           10           15
152 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Ser
153           20           25           30
155 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
156           35           40           45
158 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
159           50           55           60
161 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
162   65           70           75           80
164 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser
165           85           90           95
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169 <211> LENGTH: 325
170 <212> TYPE: DNA
171 <213> ORGANISM: Homo sapiens
173 <220> FEATURE:
174 <223> OTHER INFORMATION: light chain variable region (Vk), 10D1 from Vk
175     A-27
177 <400> SEQUENCE: 6

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178 gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
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180 cctggccagg ctcccaggct cctcatctat ggtgcattca gcagggccac tggcatccca 180
181 gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
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183 caagggacca aggtggaaat caaac 325
186 <210> SEQ ID NO: 7
187 <211> LENGTH: 108
188 <212> TYPE: PRT
189 <213> ORGANISM: Homo sapiens
191 <220> FEATURE:
192 <223> OTHER INFORMATION: light chain variagle region predicted sequence for
193 10D1 from Vk A-27
195 <400> SEQUENCE: 7
196 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
197 1 5 10 15
199 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Gly Ser Ser
200 20 25 30
202 Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
203 35 40 45
205 Ile Tyr Gly Ala Phe Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
206 50 55 60
208 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
209 65 70 75 80
211 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
212 85 90 95
214 Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
215 100 105
218 <210> SEQ ID NO: 8
219 <211> LENGTH: 325
220 <212> TYPE: DNA
221 <213> ORGANISM: Homo sapiens
223 <220> FEATURE:
224 <223> OTHER INFORMATION: light chain variable region (Vk) 4B6 from Vk A-27
226 <400> SEQUENCE: 8
227 gaaattgtgt tgacgcagtc tccaggcacc ctgtctttgt ctccagggga aagagccacc 60
228 ctctcctgca gggccagtca gagtgttagc agcagcttct tagcctggta ccagcagaaa 120
229 cctggccagg ctcccaggct cctcatctat ggtgcattca gcagggccac tggcatccca 180
230 gacaggttca gtggcagtgg gtctgggaca gacttcactc tcaccatcag cagactggag 240
231 cctgaagatt ttgcagtgtg ttactgtcag cagtatggta gctcaccgtg gacgttcggc 300
232 caagggacca aggtggaaat caaac 325
235 <210> SEQ ID NO: 9
236 <211> LENGTH: 108
237 <212> TYPE: PRT
238 <213> ORGANISM: Homo sapiens
240 <220> FEATURE:
241 <223> OTHER INFORMATION: light chain variable region predicted sequence for
242 4B6 from Vk A-27
244 <400> SEQUENCE: 9

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245 Glu Ile Val Leu Thr Gln Ser Pro Gly Thr Leu Ser Leu Ser Pro Gly
246   1           5           10           15
248 Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser
249           20           25           30
251 Phe Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu
252           35           40           45
254 Ile Tyr Gly Ala Ser Ser Arg Ala Thr Gly Ile Pro Asp Arg Phe Ser
255           50           55           60
257 Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Leu Glu
258   65           70           75           80
260 Pro Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Gly Ser Ser Pro
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268 <211> LENGTH: 287

269 <212> TYPE: DNA

270 <213> ORGANISM: Homo sapiens

272 <220> FEATURE:

273 <223> OTHER INFORMATION: Vk L-15 germline sequence

275 <400> SEQUENCE: 10

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278 gagaaagccc ctaagtccct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180
279 aggttcagcg gcagtggatc tgggacagat ttactctca ccatcagcag cctgcagcct 240
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285 <212> TYPE: PRT

286 <213> ORGANISM: Homo sapiens

288 <220> FEATURE:

289 <223> OTHER INFORMATION: light chain variable region predicted sequence for

290 Vk L-15 germline

292 <400> SEQUENCE: 11

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293 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
294   1           5           10           15
296 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Ser Trp
297           20           25           30
299 Leu Ala Trp Tyr Gln Gln Lys Pro Glu Lys Ala Pro Lys Ser Leu Ile
300           35           40           45
302 Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
303           50           55           60
305 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
306   65           70           75           80
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309           85           90

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314 <212> TYPE: DNA

VERIFICATION SUMMARY

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